conserved HECGH motif (SEQ ID NO:60) that is found, for example, in nucleotides corresponding to amino acids 105 to 109 of the *Arabidopsis* and *Brassica* delta-12 desaturase sequences, in nucleotides corresponding to amino acids 101 to 105 of the soybean delta-12 desaturase sequence and in nucleotides corresponding to amino acids 111 to 115 of the maize delta-12 desaturase sequence. See e.g., WO 94/115116; Okuley et al., Plant Cell 6:147-158 (1994). The one letter amino acid designations used herein are described in Alberts, B. et al., Molecular Biology of the Cell, 3rd edition, Garland Publishing, New York, 1994. Amino acids flanking this motif are also highly conserved among delta-12 and delta-15 desaturases and are also suitable candidates for mutations in fragments of the invention.--

Please replace the paragraph beginning at page 11, line 15 with the following rewritten paragraph:

--An illustrative embodiment of a mutation in a nucleic acid fragment of the invention is a Glu to Lys substitution in the HECGH (SEQ ID NO:60) motif of a *Brassica* microsomal delta-12 desaturase sequence, either the D form or the F form. This mutation results in the sequence HECGH (SEQ ID NO:60) being changed to HKCGH (SEQ ID NO:58) as seen by comparing amino acids 105-109 of SEQ ID NO:10 (wild-type D form) to amino acids 105-109 of SEQ ID NO:12 (mutant D form). A similar mutation in other Fad-2 sequences is contemplated to result in a non-functional gene product. (Compare SEQ ID NO:2 to SEQ ID NO:4).--

Please replace the paragraph beginning at page 11, line 32 with the following rewritten paragraph:

--Among the types of mutations in an HECGH (SEQ ID NO:60) motif that render the resulting gene product non-functional are non-conservative substitutions. An illustrative example of a non-conservative substitution is substitution of a glycine residue for either the first or second histidine. Such a substitution replaces a charged residue (histidine) with a non-polar residue (glycine). Another type of mutation that renders the

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resulting gene product non-functional is an insertion mutation, e.g., insertion of a glycine between the cysteine and glutamic acid residues in the HECGH (SEQ ID NO:60) motif.--

Please replace the paragraph beginning at page 12, line 9 with the following rewritten paragraph:

--Other regions having suitable conserved amino acid motifs include the HRRHH motif (SEQ ID NO:61) shown in Table 2, the HRTHH motif (SEQ ID NO:62) shown in Table 6 and the HVAHH motif (SEQ ID NO:63) shown in Table 3. See, e.g., WO 94/115116; Hitz, W. et al., Plant Physiol., 105:635-641 (1994); Okuley, J., et al., supra; and Yadav, N. et al., supra. An illustrative example of a mutation in the region shown in Table 3 is a mutation at nucleotides corresponding to the codon for glycine (amino acid 303 of *B. napus*). A non-conservative Gly to Glu substitution results in the amino acid sequence DRDYGILNKV (SEQ ID NO:47, amino acids 299-308 of SEQ ID NO:14) being changed to sequence DRDYEILNKV (SEQ ID NO:50, amino acids 299-308 of SEQ ID NO:18) (compare wild-type F form SEQ ID NO:14 to mutant Q4275 SEQ ID NO:18, Fig. 3).--

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Please replace the paragraph beginning at page 12, line 21 with the following rewritten paragraph:

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--Another region suitable for a mutation in a delta-12 desaturase sequence contains the motif KYLNNP (SEQ ID NO:64) at nucleotides corresponding to amino acids 170 to 175 of the *Brassica* desaturase sequence. An illustrative example of a mutation is this region is a Leu to His substitution, resulting in the amino acid sequence (Table 4) KYHNNP (SEQ ID NO:53, compare wild-type Fad2-F amino acids 170-175 of SEQ ID NO:14 to mutant Fad2-F amino acids 170-175 of SEQ ID NO:16). A similar mutation in other Fad-2 amino acid sequences is contemplated to result in a non-functional gene product. (Compare SEQ ID NO:6 to SEQ ID NO:8).--

Please replace Table 1 on page 13 with the following rewritten table:

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--**TABLE 1**

Alignment of Amino Acid Sequences from Microsomal Delta-12 Fatty Acid Desaturases

Species	Position	Amino Acid Sequence
Arabidopsis thaliana	100-129	IWVIAHECGH HAFSDYQWLD DTVGLIFHSF(SEQ ID NO:27)
Glycine max	96-125	VWVIAHECGH HAFSKYQWVD DVVGLTLHST(SEQ ID NO:28)
Zea mays	106-135	VWVIAHECGH HAFSDYSLLD DVVGLVLHSS(SEQ ID NO:29)
Ricinus communis[a]	1- 29	WVMAHDCGH HAFSDYQLLD DVVGLILHSC(SEQ ID NO:30)
Brassica napus D	100-128[b]	VWVIAHECGH HAFSDYQWLD DTVGLIFHS(SEQ ID NO:65)
Brassica napus F	100-128[c]	VWVIAHECGH HAFSDYQWLD DTVGLIFHS(SEQ ID NO:65)

[a] from plasmid pRF2-1C, [b]positions 100-128 of SEQ ID NO:10; [c]positions 100-128 of SEQ ID NO:14--

Please replace Table 2 on page 13 with the following rewritten table:

--**TABLE 2**

Alignment of Amino Acid Sequences from Microsomal Delta-12 Fatty Acid Desaturases

Species	Position	Amino Acid Sequence
Arabidopsis thaliana	130-158	LLVPYFSWKY SHRRHHSNTG SLERDEVFV(SEQ ID NO:31)
Glycine max	126-154	LLVPYFSWKI SHRRHHSNTG SLDRDEVFV(SEQ ID NO:32)
Zea mays	136-164	LMVPYFSWKY SHRRHHSNTG SLERDEVFV(SEQ ID NO:33)
Ricinus communis[a]	30- 58	LLVPYFSWKH SHRRHHSNTG SLERDEVFV(SEQ ID NO:34)
Brassica napus D	130-158[b]	LLVPYFSWKY SHRRHHSNTG SLERDEVFV(SEQ ID NO:31)
Brassica napus F	130-158[c]	LLVPYFSWKY SHRRHHSNTG SLERDEVFV(SEQ ID NO:31)

[a] from plasmid pRF2-1C; [b]positions 130-158 of SEQ ID NO:10; [c]positions 130-158 of SEQ ID NO:14--

Please replace Table 3 on page 13 with the following rewritten table:

--**TABLE 3**

Alignment of Amino Acid Sequences from Microsomal Delta-12 Fatty Acid Desaturases

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Species	Position	Amino Acid Sequence
Arabidopsis thaliana	298-333	DRDYGILNKV FHNITDTHVA HHLFSTMPHY NAMEAT(SEQ ID NO:35)
Glycine max	294-329	DRDYGILNKV FHHITDTHVA HHLFSTMPHY HAMEAT(SEQ ID NO:36)
Zea mays	305-340	DRDYGILNRV FHNITDTHVA HHLFSTMPHY HAMEAT(SEQ ID NO:37)
Ricinus communis[a]	198-224	DRDYGILNKV FHNITDTQVA HHLF TMP(SEQ ID NO:38)
Brassica napus D	299-334[b]	DRDYGILNKV FHNITDTHVA HHLFSTMPHY HAMEAT(SEQ ID NO:66)
Brassica napus F	299-334[c]	DRDYGILNKV FHNITDTHVA HHLFSTMPHY HAMEAT(SEQ ID NO:66)

[a] from plasmid pRF2-1C; [b]positions 299-334 of SEQ ID NO:10; [c]positions 299-334 of SEQ ID NO:14--

Please replace Table 4 on page 14 with the following rewritten table:

--**TABLE 4**

Alignment of Conserved Amino Acids from Microsomal Delta-12 Fatty Acid Desaturases

Species	Position	Amino Acid Sequence
Arabidopsis thaliana	165-180	IKWYGKYLNN PLGRIM(SEQ ID NO:39)
Glycine max	161-176	VAWFSLYLNN PLGRAV(SEQ ID NO:40)
Zea mays	172-187	PWYTPYVYNN PVGRVV(SEQ ID NO:41)
Ricinus communis[a]	65- 80	IRWYSKYLNN PPGRIM(SEQ ID NO:42)
Brassica napus D	165-180[b]	IKWYGKYLNN PLGRTV(SEQ ID NO:67)
Brassica napus F	165-180[c]	IKWYGKYLNN PLGRTV(SEQ ID NO:67)

[a] from plasmid pRF2-1C; [b]positions 165-180 of SEQ ID NO:10; [c]positions 165-180 of SEQ ID NO:14--

Please replace Table 5 on page 14 with the following rewritten table:

--**TABLE 5**

Alignment of Conserved Amino Acids from Plastid and Microsomal Delta-15 Fatty Acid Desaturases

Species	Position	Amino Acid Sequence
Arabidopsis thaliana[a]	156-177	WALFVLGHD CGHGSFSNDP KLN(SEQ ID NO:43)
Brassica napus[a]	114-135	WALFVLGHD CGHGSFSNDP RLN(SEQ ID NO:44)
Glycine max[a]	164-185	WALFVLGHD CGHGSFSNNS KLN(SEQ ID NO:45)
Arabidopsis thaliana	94-115	WAIFVLGHD CGHGSFSDIP LLN(SEQ ID NO:46)
Brassica napus	87-109	WALFVLGHD CGHGSFSNDP RLN(SEQ ID NO:44)
Glycine max	93-114	WALFVLGHD CGHGSFSDSP PLN(SEQ ID NO:48)

[a] Plastid sequences--

Please replace Table 6 on page 14 with the following rewritten table:

--**TABLE 6**

Alignment of Conserved Amino Acids from Plastid and Microsomal Delta-15 Fatty Acid Desaturases

Species	Position	Amino Acid Sequence
A. thaliana[a]	188-216	ILVPYHGWRI SHRTHHQNHG HVENDESWH(SEQ ID NO:49)
B. napus[a]	146-174	ILVPYHGWRI SHRTHHQNHG HVENDESWH(SEQ ID NO:49)
Glycine max[a]	196-224	ILVPYHGWRI SHRTHHQHHG HAENDESWH(SEQ ID NO:51)
A. thaliana	126-154	ILVPYHGWRI SHRTHHQNHG HVENDESWV(SEQ ID NO:52)
Brassica napus	117-145	ILVPYHGWRI SHRTHHQNHG HVENDESWV(SEQ ID NO:52)
Glycine max	125-153	ILVPYHGWRI SHRTHHQNHG HIEKDESWV(SEQ ID NO:54)

[a] Plastid sequences--

Please replace the paragraph beginning at page 17, line 1 with the following rewritten paragraph:

--The seeds of several different fatty acid lines have been deposited with the American Type Culture Collection, 10801 University Blvd., Manassas, Virginia 20110-2209, and have the following accession numbers.—

Please replace Table 20 on page 44 with the following rewritten table:

--**TABLE 20**

Alignment of Amino Acid Sequences
of Cloned Canola Membrane Bound-Desaturases

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Desaturase Gene	Sequence[a]	Position
Canola-fad2-D(mutant)	AH**K**CGH (SEQ ID NO:68)	109-114 of SEQ ID NO:12
Canola-Fad2-D	AHECGH (SEQ ID NO:69)	109-114 of SEQ ID NO:10
Canola-Fad2-F	AHECGH (SEQ ID NO:69)	109-114 of SEQ ID NO:14
Canola-FadC	GHDCAH (SEQ ID NO:55)	170-175
Canola-fad3 (mutant)	GH**K**CGH (SEQ ID NO:56)	94-99
Canola-Fad3	GHDCGH (SEQ ID NO:57)	94-99
Canola-FadD	GHDCGH (SEQ ID NO:57)	125-130

(FadD = Plastid delta 15, Fad3 = Microsomal delta-15),
(FadC = Plastid delta-12, Fad2 = Microsomal delta-12)

[a] One letter amino acid code; conservative substitutions are underlined; non-conservative substitutions are in bold.--

Please replace the paragraph beginning at page 44, line 19 with the following rewritten paragraph:

--Transcription in vivo was analyzed by RT-PCR analysis of stage II and stage III developing seeds and leaf tissue. The primers used to specifically amplify delta-12 desaturase F gene RNA from the indicated tissues were sense primer 5'-GGATATGATGATGGTGAAAGA-3' (SEQ ID NO:19) and antisense primer 5'-TCTTTCACCATCATCATATCC-3' (SEQ ID NO:20). The primers used to specifically amplify delta-12 desaturase D gene RNA from the indicated tissues were sense primer 5'-GTTATGAAGCAAAGAAGAAAC-3' (SEQ ID NO:21) and antisense primer 5'-GTTTCTTCTTTGCTTCATAAC-3' (SEQ ID NO:22). The results

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indicated that mRNA of both the D and F gene was expressed in seed and leaf tissues of IMC 129, Q508 and wild type Westar plants.--

Please replace the paragraph beginning at page 46, line 26 with the following rewritten paragraph:

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--The second plasmid, pIMC205, was prepared by inserting a mutated Fad3 gene in sense orientation into a disarmed Ti vector. The mutant sequence contained mutations at nucleotides 411 and 413 of the microsomal Fad3 gene described in WO93/11245, thus changing the sequence for codon 96 from GAC to AAG. The amino acid at codon 96 of the gene product was thereby changed from aspartic acid to lysine. See Table 20. A bean (*Phaseolus vulgaris*) phaseolin (7S seed storage protein) promoter fragment of 495 base pairs, starting with 5'-TGGTCTTTTGGT-3' (SEQ ID NO:59), was placed 5' to the mutant Fad3 gene and a phaseolin termination sequence was placed 3' to the mutant Fad3 gene. The phaseolin sequence is described in Doyle et al., (1986) J. Biol. Chem. 261:9228-9238) and Slightom et al., (1983) Proc. Natl. Acad. Sci. USA 80:1897-1901.--

Please replace the paragraph beginning at page 49, line 5 with the following rewritten paragraph:

C9

--The Fad2-D gene was amplified once using Elongase® (Gibco-BRL). PCR primers were: 5'-CAUCAUCAUCAUCTTCTTCGTAGGGTTCATCG-3' (SEQ ID NO:23) and 5'-CUACUACUACUATCATAGAAGAGAAAGGTTCAG-3' (SEQ ID NO:24) for the 5' and 3' ends of the gene, respectively.--

Please replace the paragraph beginning at page 49, line 10 with the following rewritten paragraph:

--The Fad2-F gene was independently amplified 4 times, twice with Elongase® and twice with Taq polymerase (Boehringer Mannheim). The PCR primers used were: 5'CAUCAUCAUCAUCATGGGTGCACGTGGAAGAA3' (SEQ ID NO:25) and

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5'CUACUACUACUATCTTTCACCATCATCATATCC3' (SEQ ID NO:26) for the 5' and 3' ends of the gene, respectively.--

Please replace the sequence listing in the application with the substitute sequence listing submitted herewith.